



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/935,625

DATE: 05/21/2002

TIME: 15:01:16

Input Set : N:\paola\PTO.PG.txt

Output Set: N:\CRF3\05212002\I935625.raw

p5

3 <110> APPLICANT: N. ALEXANDROV et al.
 5 <120> TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF
 CAPABLE OF

6 MODULATING VARIOUS RESPONSES

8 <130> FILE REFERENCE: 2750-1481P

10 <140> CURRENT APPLICATION NUMBER: 09/935,625

11 <141> CURRENT FILING DATE: 2001-08-24

13 <160> NUMBER OF SEQ ID NOS: 33136

15 <210> SEQ ID NO: 1

16 <211> LENGTH: 1568

17 <212> TYPE: DNA

18 <213> ORGANISM: Arabidopsis thaliana

20 <220> FEATURE:

21 <221> NAME/KEY: Misc_feature

22 <222> LOCATION: 1..1568

23 <223> OTHER INFORMATION: Ceres Seq. ID no. 1008285

25 <400> SEQUENCE: 1

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| 27 | ttggtttttct | cattttccgaa | atataaaaag | atggccaaag | cgccaccgtc | aatctctctt | 120 |
| 28 | ctcctcctcc | tctgcgcgcg | cgtattcctc | accatccccg | ccgtgatctc | cgccatcggt | 180 |
| 29 | gttaactacg | gaactctcgg | aaacctccca | ccaccgaactc | aggtggctaa | ctttatcaag | 240 |
| 30 | acacaaactt | cgattgataa | cgtcaagatc | ttcgatgtga | atcccgatat | cctacgtgcc | 300 |
| 31 | ttcgctggaa | ctggtatctc | cgtcgttggtc | accgttccta | acggtgatat | tccggcggtg | 360 |
| 32 | gctaaccgga | gacaagctcg | tcggtgggtt | tcggttaaca | ttttgccgtt | tcctcctcag | 420 |
| 33 | acgaagatta | agtatatctc | agtcggaaat | gagattctgc | tcaccggaga | taataacatg | 480 |
| 34 | atcaataatc | tcttaccggc | gatgagggaat | cttaacaacg | ctttgggttcg | tgctgggtgc | 540 |
| 35 | agagatgtta | aggttacaac | cgcacactca | cttaacatca | tagcctatga | cctgaccggt | 600 |
| 36 | gcaccaagca | gcggtagatt | caggccgggt | tgggacaaag | gcatattggc | tccaatccta | 660 |
| 37 | gcttaccatc | gccgaaccaa | gtctcctttc | atggttaacc | cgtaccctta | ctttgggttt | 720 |
| 38 | gaccccaaaa | acgtcaactt | cgcaattttc | cgaacaccgt | acaaggcagt | ccgtgaccgc | 780 |
| 39 | ttcaccgcc | acgtctacac | caacatgttt | gatgcactca | tggactcgac | atactcagcc | 840 |
| 40 | atgaaagctc | ttggatacgg | tgatgttaac | attgtcgttg | gcgagactgg | ctggccatct | 900 |
| 41 | gcttgtgacg | caccttggtg | ctcgcctgcg | aatgctgctt | ggttcaacct | caacattatc | 960 |
| 42 | aaacgtgcac | aaggccaagg | gacacctctc | atgcctaaca | gacggttcga | gacatacatt | 1020 |
| 43 | ttcggctctc | tcaacgaaga | aggcaaacc | ggtccgaccg | cagagcgtaa | ctggggactt | 1080 |
| 44 | ttccgagcag | attttctccc | ggtttacgat | gttggtcttc | tccgaaacgg | acaaggcggt | 1140 |
| 45 | ggaggccgcc | cagcattgcc | cgcacctagt | actgcgcggc | gtaaatggtg | tgtagcgagg | 1200 |
| 46 | tccggggcga | cgaataactca | gctgcaagac | agtattaatt | gggtgtgtgg | tcagggtggt | 1260 |
| 47 | gactgtaaac | cgatccaagc | tggtgtgttcg | tgctttaacc | cgagcagttt | gaggacgcac | 1320 |
| 48 | gcatcttttg | ttatgaatgc | ttatttccag | agccacggcc | gcactgatgg | tgcttgtaac | 1380 |
| 49 | ttcagtggaa | ctggtatgat | cgtaggggaac | aacccaagca | atggtgcatg | taagtactaa | 1440 |
| 50 | ggagattgtc | tatgtagtag | tatttgtctg | gaaagtccta | acataatggt | tctgagggaac | 1500 |
| 51 | tttggatttg | agagatcatc | agctttgtgt | ttaatttcgg | attatcctaa | ttttaagatt | 1560 |
| 52 | ttttgtc | | | | | | 1568 |

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54 <210> SEQ ID NO: 2
55 <211> LENGTH: 479
56 <212> TYPE: PRT
57 <213> ORGANISM: Arabidopsis thaliana
59 <220> FEATURE:
60 <221> NAME/KEY: peptide
61 <222> LOCATION: 1..479
62 <223> OTHER INFORMATION: Ceres Seq. ID no. 1008286
64 <400> SEQUENCE: 2
65 Leu Phe Val Val Ile Ile Lys Thr Gln Leu Lys Arg Phe Thr Gly Phe
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67 Thr Trp Asn Arg Leu Val Phe Ser Phe Pro Lys Tyr Lys Lys Met Ala
68 20 25 30
69 Lys Ala Pro Pro Ser Ile Ser Leu Leu Leu Leu Cys Ala Ala Val
70 35 40 45
71 Phe Leu Thr Ile Pro Ala Val Ile Ser Ala Ile Gly Val Asn Tyr Gly
72 50 55 60
73 Thr Leu Gly Asn Leu Pro Pro Thr Gln Val Ala Asn Phe Ile Lys
74 65 70 75 80
75 Thr Gln Thr Ser Ile Asp Asn Val Lys Ile Phe Asp Val Asn Pro Asp
76 85 90 95
77 Ile Leu Arg Ala Phe Ala Gly Thr Gly Ile Ser Val Val Val Thr Val
78 100 105 110
79 Pro Asn Gly Asp Ile Pro Ala Leu Ala Asn Gly Arg Gln Ala Arg Arg
80 115 120 125
81 Trp Val Ser Val Asn Ile Leu Pro Phe His Pro Gln Thr Lys Ile Lys
82 130 135 140
83 Tyr Ile Ser Val Gly Asn Glu Ile Leu Leu Thr Gly Asp Asn Asn Met
84 145 150 155 160
85 Ile Asn Asn Leu Leu Pro Ala Met Arg Asn Leu Asn Asn Ala Leu Val
86 165 170 175
87 Arg Ala Gly Val Arg Asp Val Lys Val Thr Thr Ala His Ser Leu Asn
88 180 185 190
89 Ile Ile Ala Tyr Asp Leu Thr Gly Ala Pro Ser Ser Gly Arg Phe Arg
90 195 200 205
91 Pro Gly Trp Asp Lys Gly Ile Leu Ala Pro Ile Leu Ala Tyr His Arg
92 210 215 220
93 Arg Thr Lys Ser Pro Phe Met Val Asn Pro Tyr Pro Tyr Phe Gly Phe
94 225 230 235 240
95 Asp Pro Lys Asn Val Asn Phe Ala Ile Phe Arg Thr Pro Tyr Lys Ala
96 245 250 255
97 Val Arg Asp Pro Phe Thr Arg His Val Tyr Thr Asn Met Phe Asp Ala
98 260 265 270
99 Leu Met Asp Ser Thr Tyr Ser Ala Met Lys Ala Leu Gly Tyr Gly Asp
100 275 280 285
101 Val Asn Ile Val Val Gly Glu Thr Gly Trp Pro Ser Ala Cys Asp Ala
102 290 295 300
103 Pro Trp Cys Ser Pro Ala Asn Ala Ala Trp Phe Asn Leu Asn Ile Ile
104 305 310 315 320

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105 Lys Arg Ala Gln Gly Gln Gly Thr Pro Leu Met Pro Asn Arg Arg Phe
106           325           330           335
107 Glu Thr Tyr Ile Phe Gly Leu Phe Asn Glu Glu Gly Lys Pro Gly Pro
108           340           345           350
109 Thr Ala Glu Arg Asn Trp Gly Leu Phe Arg Ala Asp Phe Ser Pro Val
110           355           360           365
111 Tyr Asp Val Gly Leu Leu Arg Asn Gly Gln Gly Gly Gly Arg Pro
112           370           375           380
113 Ala Leu Pro Ala Pro Ser Thr Ala Gly Gly Lys Trp Cys Val Ala Arg
114 385           390           395           400
115 Ser Gly Ala Thr Asn Thr Gln Leu Gln Asp Ser Ile Asn Trp Val Cys
116           405           410           415
117 Gly Gln Gly Val Asp Cys Lys Pro Ile Gln Ala Gly Gly Ser Cys Phe
118           420           425           430
119 Asn Pro Ser Ser Leu Arg Thr His Ala Ser Phe Val Met Asn Ala Tyr
120           435           440           445
121 Phe Gln Ser His Gly Arg Thr Asp Gly Ala Cys Asn Phe Ser Gly Thr
122           450           455           460
123 Gly Met Ile Val Gly Asn Asn Pro Ser Asn Gly Ala Cys Lys Tyr
124 465           470           475
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 449
128 <212> TYPE: PRT
129 <213> ORGANISM: Arabidopsis thaliana
131 <220> FEATURE:
132 <221> NAME/KEY: peptide
133 <222> LOCATION: 1..449
134 <223> OTHER INFORMATION: Ceres Seq. ID no. 1008287
136 <400> SEQUENCE: 3
137 Met Ala Lys Ala Pro Pro Ser Ile Ser Leu Leu Leu Leu Cys Ala
138 1           5           10           15
139 Ala Val Phe Leu Thr Ile Pro Ala Val Ile Ser Ala Ile Gly Val Asn
140           20           25           30
141 Tyr Gly Thr Leu Gly Asn Leu Pro Pro Thr Gln Val Ala Asn Phe
142           35           40           45
143 Ile Lys Thr Gln Thr Ser Ile Asp Asn Val Lys Ile Phe Asp Val Asn
144           50           55           60
145 Pro Asp Ile Leu Arg Ala Phe Ala Gly Thr Gly Ile Ser Val Val Val
146 65           70           75           80
147 Thr Val Pro Asn Gly Asp Ile Pro Ala Leu Ala Asn Gly Arg Gln Ala
148           85           90           95
149 Arg Arg Trp Val Ser Val Asn Ile Leu Pro Phe His Pro Gln Thr Lys
150           100           105           110
151 Ile Lys Tyr Ile Ser Val Gly Asn Glu Ile Leu Leu Thr Gly Asp Asn
152           115           120           125
153 Asn Met Ile Asn Asn Leu Leu Pro Ala Met Arg Asn Leu Asn Asn Ala
154           130           135           140
155 Leu Val Arg Ala Gly Val Arg Asp Val Lys Val Thr Thr Ala His Ser
156 145           150           155           160

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157 Leu Asn Ile Ile Ala Tyr Asp Leu Thr Gly Ala Pro Ser Ser Gly Arg
158                               165                170                175
159 Phe Arg Pro Gly Trp Asp Lys Gly Ile Leu Ala Pro Ile Leu Ala Tyr
160                               180                185                190
161 His Arg Arg Thr Lys Ser Pro Phe Met Val Asn Pro Tyr Pro Tyr Phe
162                               195                200                205
163 Gly Phe Asp Pro Lys Asn Val Asn Phe Ala Ile Phe Arg Thr Pro Tyr
164                               210                215                220
165 Lys Ala Val Arg Asp Pro Phe Thr Arg His Val Tyr Thr Asn Met Phe
166 225                               230                235                240
167 Asp Ala Leu Met Asp Ser Thr Tyr Ser Ala Met Lys Ala Leu Gly Tyr
168                               245                250                255
169 Gly Asp Val Asn Ile Val Val Gly Glu Thr Gly Trp Pro Ser Ala Cys
170                               260                265                270
171 Asp Ala Pro Trp Cys Ser Pro Ala Asn Ala Ala Trp Phe Asn Leu Asn
172                               275                280                285
173 Ile Ile Lys Arg Ala Gln Gly Gln Gly Thr Pro Leu Met Pro Asn Arg
174                               290                295                300
175 Arg Phe Glu Thr Tyr Ile Phe Gly Leu Phe Asn Glu Glu Gly Lys Pro
176 305                               310                315                320
177 Gly Pro Thr Ala Glu Arg Asn Trp Gly Leu Phe Arg Ala Asp Phe Ser
178                               325                330                335
179 Pro Val Tyr Asp Val Gly Leu Leu Arg Asn Gly Gln Gly Gly Gly Gly
180                               340                345                350
181 Arg Pro Ala Leu Pro Ala Pro Ser Thr Ala Gly Gly Lys Trp Cys Val
182                               355                360                365
183 Ala Arg Ser Gly Ala Thr Asn Thr Gln Leu Gln Asp Ser Ile Asn Trp
184                               370                375                380
185 Val Cys Gly Gln Gly Val Asp Cys Lys Pro Ile Gln Ala Gly Gly Ser
186 385                               390                395                400
187 Cys Phe Asn Pro Ser Ser Leu Arg Thr His Ala Ser Phe Val Met Asn
188                               405                410                415
189 Ala Tyr Phe Gln Ser His Gly Arg Thr Asp Gly Ala Cys Asn Phe Ser
190                               420                425                430
191 Gly Thr Gly Met Ile Val Gly Asn Asn Pro Ser Asn Gly Ala Cys Lys
192                               435                440                445
193 Tyr
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 320
198 <212> TYPE: PRT
199 <213> ORGANISM: Arabidopsis thaliana
201 <220> FEATURE:
202 <221> NAME/KEY: peptide
203 <222> LOCATION: 1..320
204 <223> OTHER INFORMATION: Ceres Seq. ID no. 1008288
206 <400> SEQUENCE: 4
207 Met Ile Asn Asn Leu Leu Pro Ala Met Arg Asn Leu Asn Asn Ala Leu
208 1                               5                10                15
209 Val Arg Ala Gly Val Arg Asp Val Lys Val Thr Thr Ala His Ser Leu

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210          20          25          30
211 Asn Ile Ile Ala Tyr Asp Leu Thr Gly Ala Pro Ser Ser Gly Arg Phe
212          35          40          45
213 Arg Pro Gly Trp Asp Lys Gly Ile Leu Ala Pro Ile Leu Ala Tyr His
214          50          55          60
215 Arg Arg Thr Lys Ser Pro Phe Met Val Asn Pro Tyr Pro Tyr Phe Gly
216 65          70          75          80
217 Phe Asp Pro Lys Asn Val Asn Phe Ala Ile Phe Arg Thr Pro Tyr Lys
218          85          90          95
219 Ala Val Arg Asp Pro Phe Thr Arg His Val Tyr Thr Asn Met Phe Asp
220          100          105          110
221 Ala Leu Met Asp Ser Thr Tyr Ser Ala Met Lys Ala Leu Gly Tyr Gly
222          115          120          125
223 Asp Val Asn Ile Val Val Gly Glu Thr Gly Trp Pro Ser Ala Cys Asp
224          130          135          140
225 Ala Pro Trp Cys Ser Pro Ala Asn Ala Ala Trp Phe Asn Leu Asn Ile
226 145          150          155          160
227 Ile Lys Arg Ala Gln Gly Gln Gly Thr Pro Leu Met Pro Asn Arg Arg
228          165          170          175
229 Phe Glu Thr Tyr Ile Phe Gly Leu Phe Asn Glu Glu Gly Lys Pro Gly
230          180          185          190
231 Pro Thr Ala Glu Arg Asn Trp Gly Leu Phe Arg Ala Asp Phe Ser Pro
232          195          200          205
233 Val Tyr Asp Val Gly Leu Leu Arg Asn Gly Gln Gly Gly Gly Arg
234          210          215          220
235 Pro Ala Leu Pro Ala Pro Ser Thr Ala Gly Gly Lys Trp Cys Val Ala
236 225          230          235          240
237 Arg Ser Gly Ala Thr Asn Thr Gln Leu Gln Asp Ser Ile Asn Trp Val
238          245          250          255
239 Cys Gly Gln Gly Val Asp Cys Lys Pro Ile Gln Ala Gly Gly Ser Cys
240          260          265          270
241 Phe Asn Pro Ser Ser Leu Arg Thr His Ala Ser Phe Val Met Asn Ala
242          275          280          285
243 Tyr Phe Gln Ser His Gly Arg Thr Asp Gly Ala Cys Asn Phe Ser Gly
244          290          295          300
245 Thr Gly Met Ile Val Gly Asn Asn Pro Ser Asn Gly Ala Cys Lys Tyr
246 305          310          315          320
249 <210> SEQ ID NO: 5
250 <211> LENGTH: 427
251 <212> TYPE: DNA
252 <213> ORGANISM: Arabidopsis thaliana
254 <220> FEATURE:
255 <221> NAME/KEY: Misc_feature
256 <222> LOCATION: 1..427
257 <223> OTHER INFORMATION: Ceres Seq. ID no. 1008330
259 <400> SEQUENCE: 5
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261 tggagatggtt ggaagagtac aagaggctag cgaagatatg gagcaagatg aaaggactca 120
262 agatcccaaa gaatggagat atgagtgcac tctcgagaaa catgaacgca cagcacatga 180

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.